```
RESULT 6
HUMIRGT
LOCUS       HUMIRGT                 2128 bp    mRNA    linear   PRI 06-JAN-1995
DEFINITION  Human insulin-responsive glucose transporter (GLUT4) mRNA, complete
            cds.
ACCESSION   M20747
VERSION     M20747.1  GI:186552
KEYWORDS    insulin-responsive glucose transporter.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2128)
  AUTHORS   Fukumoto,H., Kayano,T., Buse,J.B., Edwards,Y., Pilch,P.F.,
            Bell,G.I. and Seino,S.
  TITLE     Cloning and characterization of the major insulin-responsive
            glucose transporter expressed in human skeletal muscle and other
            insulin-responsive tissues
  JOURNAL   J. Biol. Chem. 264 (14), 7776-7779 (1989)
   PUBMED   2656669
COMMENT     Original source text: Human jejunum and muscle, cDNA to mRNA,
            clones lambda-h-[JHT-3, AMT-6, FMT-1].
            Draft entry and computer-readable sequence for [1] kindly provided
            by G.I.Bell, 19-APR-1989.
FEATURES             Location/Qualifiers
     source          1. .2128
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     CDS             146. .1675
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                     /db_xref="GDB:G00-119-997"
                     /translation="MPSGFQQIGSEDGEPPQQRVTGTLVLAVFSAVLGSLQFGYNIGV
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                     SQWLGRKRAMLVNNVLAVLGGSLMGLANAAASYEMLILGRFLIGAYSGLTSGLVPMYV
                     GEIAPTHLRGALGTLNQLAIVIGILIAQVLGLESLLGTASLWPLLLGLTVLPALLQLV
                     LLPFCPESPRYLYIIQNLEGPARKSLKRLTGWADVSGVLAELKDEKRKLERERPLSLL
                     QLLGSRTHRQPLIIAVVLQLSQQLSGINAVFYYSTSIFETAGVGQPAYATIGAGVVNT
                     VFTLVSVLLVERAGRRTLHLLGLAGMCGCAILMTVALLLLERVPAMSYVSIVAIFGFV
                     AFFEIGPGPIPWFIVAELFSQGPRPAAMAVAGFSNWTSNFIIGMGFQYVAEAMGPYVF
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                     D"
ORIGIN

  Query Match             99.9%;  Score 1528.4;  DB 8;  Length 2128;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1529;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCCGTCGGGCTTCCAACAGATAGGCTCCGAAGATGGGGAACCCCCTCAGCAGCGAGTG 60
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Db        146 ATGCCGTCGGGCTTCCAACAGATAGGCTCCGAAGATGGGGAACCCCCTCAGCAGCGAGTG 205

Qy         61 ACTGGGACCCTGGTCCTTGCTGTGTTCTCTGCGGTGCTTGGCTCCCTGCAGTTTGGGTAC 120
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Db        206 ACTGGGACCCTGGTCCTTGCTGTGTTCTCTGCGGTGCTTGGCTCCCTGCAGTTTGGGTAC 265

Qy        121 AACATTGGGGTCATCAATGCCCCTCAGAAGGTGATTGAACAGAGCTACAATGAGACGTGG 180
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Db        326 CTGGGGAGGCAGGGGCCTGAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTC 385

Qy        241 TGGGCCCTCTCCATGGCCATCTTTTCCGTGGGCGGCATGATTTCCTCCTTCCTCATTGGT 300
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Db        446 ATCATCTCTCAGTGGCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTG 505

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Db        806 CCCTTCTGTCCCGAGAGCCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCCTGCC 865

Qy        721 AGAAAGAGTCTGAAGCGCCTGACAGGCTGGGCCGATGTTTCTGGAGTGCTGGCTGAGCTG 780
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Qy       1141 AGCTACGTCTCCATTGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGC 1200
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Qy       1321 GTTGCGGAGGCTATGGGGCCCTACGTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCTTC 1380
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Qy       1381 TTCATCTTCACCTTCTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAGATCTCA 1440
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RESULT 10
AEB32290
ID   AEB32290 standard; cDNA; 2128 BP.
XX
AC   AEB32290;
XX
DT   08-SEP-2005  (first entry)
XX
DE   Human cDNA #53.
XX
KW   SNP detection; diagnosis; non-insulin dependent diabetes; obesity;
KW   antidiabetic; anorectic; endocrine disease; gastrointestinal disease;
KW   metabolic disorder; nutritional disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2005147987-A1.
XX
PD   07-JUL-2005.
XX
PF   19-JUL-2004; 2004US-00893315.
XX
PR   08-SEP-2000; 2000US-0231397P.
PR   10-SEP-2001; 2001US-00948947.
XX
PA   (APPL-) APPLERA CORP NY.
XX
PI   Venter JC,  Zhang JN,  Liu X,  Rowe W,  Cravchik A,  Kalush F;
PI   Naik A,  Subramanian G,  Woodage T;
XX
DR   WPI; 2005-511776/52.
DR   P-PSDB; AEB32351.
XX
PT   New detection reagent capable of detecting 1, 100, 500, 1000 or 5000 or
PT   more single nucleic acid polymorphisms, useful in identifying an
PT   individual having or at risk of developing type II diabetes or obesity.
XX
PS   Disclosure; SEQ ID NO 53; 31pp; English.
XX
CC   The invention relates to a detection reagent capable of detecting one or
CC   more single nucleic acid polymorphisms. The invention also relates to
CC   determining whether a trait is linked to one of the human chromosomes or
CC   its sub-region, a computer readable medium having stored in it the SNP
CC   relational information given in the specification, an isolated nucleic
CC   acid molecule for detecting at least one SNP given in the specification
CC   comprising at least about 12 contiguous nucleotides, genotyping at least
CC   one SNP position given in the specification in a sample, identifying an
CC   individual having or at risk of developing a disorder and a kit
CC   comprising at least one container containing the detection reagent.
CC   Determining whether a trait is linked to one of the human chromosomes or
CC   its sub-region comprises determining whether the trait is linked to one
CC   or more SNPs using the detection reagents. Genotyping at least one SNP
CC   position given in the specification in a sample comprises contacting the
CC   sample with a detection reagent that differentiates between alternative
CC   alleles at at least one SNP position given in the specification, and
CC   determining which allele is present at the at least one SNP position.
CC   Identifying an individual having or at risk of developing a disorder
CC   comprises genotyping at least one SNP given in the specification in a
CC   nucleic acid sample from the individual. The disorder is type II diabetes
CC   (non-insulin dependent diabetes) or obesity. The detection reagent is
CC   useful in identifying an individual having or at risk of developing a
CC   disorder, particularly type II diabetes or obesity. This sequence
CC   represents human cDNA used in the scope of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification but was obtained in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 2128 BP; 362 A; 663 C; 600 G; 503 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1526.8;  DB 14;  Length 2128;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1528;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCCGTCGGGCTTCCAACAGATAGGCTCCGAAGATGGGGAACCCCCTCAGCAGCGAGTG 60
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Qy         61 ACTGGGACCCTGGTCCTTGCTGTGTTCTCTGCGGTGCTTGGCTCCCTGCAGTTTGGGTAC 120
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102(e)

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Db       266 AACATTGGGGTCATCAATGCCCCTCAGAAGGTGATTGAACAGAGCTACAATGAGACGTGG 325

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Db       446 ATCATCTCTCAGTGGCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTG 505

Qy       361 CTGGGGGGCAGCCTCATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTT 420
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Qy       421 GGACGATTCCTCATTGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTG 480
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Qy       541 GTTATCGGCATTCTGATCGCCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       686 GTTATCGGCATTCTGATCGCCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGC 745

Qy       601 CTGTGGCCACTGCTCCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCCTGCTG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       746 CTGTGGCCACTGCTCCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCCTGCTG 805

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1021 GTGTTGTTGGTGGAGCGGGCGGGGCGCCGGACGCTCCATCTCCTGGGCCTGGCGGGCATG 1080
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Qy      1081 TGTGGCTGTGCCATCCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATG 1140
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Qy      1141 AGCTACGTCTCCATTGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGC 1200
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Db      1286 AGCTACGTCTCCATTGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGC 1345

Qy      1201 CCCATTCCTTGGTTCATCGTGGCCGAGCTCTTCAGCCAGGGACCCCGCCCGGCAGCCATG 1260
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Qy      1261 GCTGTGGCTGGTTTCTCCAACTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTAT 1320
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Qy      1321 GTTGCGGAGGCTATGGGGCCCTACGTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCTTC 1380
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Met → Val

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RESULT 1
US-09-591-025-8
; Sequence 8, Application US/09591025
; Patent No. 6303373
; GENERAL INFORMATION:
;  APPLICANT:  Bogan, Jonathan S.
;  APPLICANT:  Lodish, Harvey F.
;  TITLE OF INVENTION:  Method of Measuring Plasma Membrane
;  TITLE OF INVENTION:  Targeting of GLUT4
;  FILE REFERENCE:  0399.1210-004
;  CURRENT APPLICATION NUMBER: US/09/591,025
;  CURRENT FILING DATE:  2000-06-09
;  PRIOR APPLICATION NUMBER:  60/154,078
;  PRIOR FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER:  60/138,237
;  PRIOR FILING DATE:  1999-06-09
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 2592
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified GLUT4 containing myc tag sequences
US-09-591-025-8

  Query Match           86.6%;  Score 1325;  DB 3;  Length 2592;
  Best Local Similarity  99.6%;  Pred. No. 0;
  Matches 1328;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        195 GCCTGAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTCTGGGCCCTCTCCAT 254
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 GGCCATCTTTTCCGTGGGCGGCATGATTTCCTCCTTCCTCATTGGTATCATCTCTCAGTG 629

Qy        315 GCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTGCTGGGGGGCAGCCT 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 GCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTGCTGGGGGGCAGCCT 689

Qy        375 CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCCTCAT 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCCTCAT 749

Qy        435 TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC 809

Qy        495 CACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 CACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT 869

Qy        555 GATCGCCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 GATCGCCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT 929

Qy        615 CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCCTGCTGCCCTTCTGTCCCGA 674
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Db        930 CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCCTGCTGCCCTTCTGTCCCGA 989

Qy        675 GAGCCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCCTGCCAGAAAGAGTCTGAA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 GAGCCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCCTGCCAGAAAGAGTCTGAA 1049

Qy        735 GCGCCTGACAGGCTGGGCCGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 GCGCCTGACAGGCTGGGCCGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG 1109

Qy        795 GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG 1169

Qy        855 GCAGCCCCTGATCATTGCGGTCGTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC 914
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Qy        915 TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC 974
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LOW SCORE

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Qy        975 CACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCGGTGTTGTTGGTGGA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 CACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCGGTGTTGTTGGTGGA 1349

Qy       1035 GCGGGCGGGGCGCCGGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1350 GCGGGCGGGGCGCCGGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT 1409

Qy       1095 CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATGAGCTACGTCTCCAT 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1410 CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATGAGCTACGTCTCCAT 1469

Qy       1155 TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGCCCCATTCCTTGGTT 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1470 TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGCCCCATTCCTTGGTT 1529

Qy       1215 CATCGTGGCCGAGCTCTTCAGCCAGGGACCCCGCCCGGCAGCCATGGCTGTGGCTGGTTT 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 CATCGTGGCCGAGCTCTTCAGCCAGGGACCCCGCCCGGCAGCCATGGCTGTGGCTGGTTT 1589

Qy       1275 CTCCAACTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT 1334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 CTCCAACTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT 1649

Qy       1335 GGGGCCCTACGTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCTTCTTCATCTTCACCTT 1394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 GGGGCCCTACGTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCTTCTTCATCTTCACCTT 1709

Qy       1395 CTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAGATCTCAGCTGCCTTCCACCG 1454
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1710 CTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAGATCTCGGCTGCCTTCCACCG 1769

Qy       1455 GACACCCTCTCTTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC 1514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1770 GACACCCTCTCTTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC 1829

Qy       1515 AGATGAGAACGAC 1527
              ||||||||| |||
Db       1830 AGATGAGAATGAC 1842
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RESULT 2
US-09-894-927B-8
; Sequence 8, Application US/09894927B
; Patent No. 6632924
; GENERAL INFORMATION:
;  APPLICANT: Bogan, Jonathan S.
;  APPLICANT:  Lodish, Harvey F.
;  TITLE OF INVENTION: Method of Measuring Plasma Membrane
;  TITLE OF INVENTION:  Targeting of GLUT4
;  FILE REFERENCE: 0399.1210-005
;  CURRENT APPLICATION NUMBER: US/09/894,927B
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/591,025
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: US 60/154,078
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: US 60/138,237
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 2592
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified GLUT4 containing myc tag sequences
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(2592)
US-09-894-927B-8

  Query Match             86.4%;  Score 1321.8;  DB 3;  Length 2592;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 1326;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        195 GCCTGAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTCTGGGCCCTCTCCAT 254
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Db        510 GCTTAAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTCTGGGCCCTCTCCGT 569
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Qy       255 GGCCATCTTTTCCGTGGGCGGCATGATTTCCTCCTTCCTCATTGGTATCATCTCTCAGTG 314
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Qy       315 GCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTGCTGGGGGGCAGCCT 374
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Db       630 GCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGCTCTGGCGGTGCTGGGGGGCAGCCT 689

Qy       375 CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCCTCAT 434
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Db       690 CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCCTCAT 749

Qy       435 TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC 494
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Db       750 TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC 809

Qy       495 CACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT 554
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Db       810 CACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT 869

Qy       555 GATCGCCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT 614
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Db       870 GATCGCCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT 929

Qy       615 CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCCTGCTGCCCTTCTGTCCCGA 674
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Qy       675 GAGCCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCCTGCCAGAAAGAGTCTGAA 734
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Db       990 GAGCCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCCTGCCAGAAAGAGTCTGAA 1049

Qy       735 GCGCCTGACAGGCTGGGCCGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG 794
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Qy       795 GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG 854
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Qy       855 GCAGCCCCTGATCATTGCGGTCGTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC 914
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Qy       915 TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC 974
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Db      1230 TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC 1289

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Db      1350 GCGGGCGGGGCGCCGGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT 1409

Qy      1095 CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATGAGCTACGTCTCCAT 1154
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1410 CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATGAGCTACGTCTCCAT 1469

Qy      1155 TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGCCCCATTCCTTGGTT 1214
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Qy      1215 CATCGTGGCCGAGCTCTTCAGCCAGGGACCCCGCCCGGCAGCCATGGCTGTGGCTGGTTT 1274
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Qy      1275 CTCCAACTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT 1334
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Qy      1335 GGGGCCCTACGTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCTTCTTCATCTTCACCTT 1394
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Qy      1455 GACACCCTCTCTTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC 1514
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1770 GACACCCTCTCTTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC 1829

Qy        1515 AGATGAGAACGAC 1527
                ||||||||| |||
Db        1830 AGATGAGAATGAC 1842
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RESULT 14
ABL41106
ID   ABL41106 standard; DNA; 2592 BP.
XX
AC   ABL41106;
XX
DT   12-AUG-2002  (first entry)
XX
DE   Modified GLUT4 encoding nucleotide sequence.
XX
KW   Protein translocation; plasma membrane; GLUT-4; diabetes mellitus;
KW   insulin; gene; GFP; green fluorescent protein; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2592
FT                   /*tag=  a
FT                   /product= "modified GLUT4"
FT                   /note= "contains myc epitope tags and GFP"
FT   misc_feature    1873. .2592
FT                   /*tag=  b
FT                   /note= "GFP"
XX
PN   US2002052012-A1.
XX
PD   02-MAY-2002.
XX
PF   28-JUN-2001; 2001US-00894927.
XX
PR   22-MAY-1997;   97US-0047433P.
PR   09-JUN-1999;   99US-0138237P.
PR   15-SEP-1999;   99US-0154078P.
PR   09-JUN-2000; 2000US-00591025.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Bogan JS,  Lodish HF;
XX
DR   WPI; 2002-443696/47.
DR   P-PSDB; ABB07975.
XX
PT   Determining protein translocation to the plasma membrane of a mammalian
PT   cell using a modified protein with an intracellular fluorescent tag and
PT   an extracellular group tag, useful in finding new drugs, particularly to
PT   treat diabetes.
XX
PS   Example 1; Fig 8a-b; 34pp; English.
XX
CC   The invention relates to determining if a protein translocates from an
CC   intracellular location to the plasma membrane of a mammalian cell in the
CC   presence of a condition or stimulus. The method involves modifying the
CC   protein with a group tag in the extracellular domain and a fluorescent
CC   tag in the intracellular domain and determining the proportion of total
CC   protein which is at the membrane. The method is used to identify a drug
CC   which enhances translocation of a protein from an intracellular location
CC   to the plasma membrane of a mammalian cell. The method is particularly
CC   used to measure GLUT-4 protein translocation to identify drugs to treat
CC   insulin resistance in adult-onset diabetes mellitus. The invention
CC   provides a less labour intensive quantitative method for measuring GLUT4
CC   translocation than prior art methods. The present sequence represents a
CC   modified GLUT4 nucleotide sequence, containing myc epiotpe tags and green
CC   fluorescent protein (GFP) sequences
XX
SQ   Sequence 2592 BP; 545 A; 767 C; 733 G; 547 T; 0 U; 0 Other;

  Query Match           86.6%;  Score 1325;  DB 6;  Length 2592;
  Best Local Similarity  99.6%;  Pred. No. 3.2e-314;
  Matches 1328;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        195 GCCTGAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTCTGGGCCCTCTCCAT 254
              || | ||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        510 GCTTAAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTCTGGGCCCTCTCCGT 569

Qy        255 GGCCATCTTTTCCGTGGGCGGCATGATTTCCTCCTTCCTCATTGGTATCATCTCTCAGTG 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        315 GCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTGCTGGGGGGCAGCCT 374
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Db        630 GCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTGCTGGGGGGCAGCCT 689
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Low score

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Db       690 CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCCTCAT 749

Qy       435 TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC 494
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       750 TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC 809

Qy       495 CACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT 554
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Db       810 CACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT 869

Qy       555 GATCGCCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT 614
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       870 GATCGCCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT 929

Qy       615 CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCCTGCTGCCCTTCTGTCCCGA 674
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       930 CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCCTGCTGCCCTTCTGTCCCGA 989

Qy       675 GAGCCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCCTGCCAGAAAGAGTCTGAA 734
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       990 GAGCCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCCTGCCAGAAAGAGTCTGAA 1049

Qy       735 GCGCCTGACAGGCTGGGCCGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG 794
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1050 GCGCCTGACAGGCTGGGCCGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG 1109

Qy       795 GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG 854
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1110 GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG 1169

Qy       855 GCAGCCCCTGATCATTGCGGTCGTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC 914
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1170 GCAGCCCCTGATCATTGCGGTCGTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC 1229

Qy       915 TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC 974
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Db      1230 TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC 1289

Qy       975 CACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCGGTGTTGTTGGTGGA 1034
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Qy      1035 GCGGGCGGGGCGCCGGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT 1094
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Db      1350 GCGGGCGGGGCGCCGGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT 1409

Qy      1095 CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATGAGCTACGTCTCCAT 1154
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1410 CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATGAGCTACGTCTCCAT 1469

Qy      1155 TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGCCCCATTCCTTGGTT 1214
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Qy      1215 CATCGTGGCCGAGCTCTTCAGCCAGGGACCCCGCCCGGCAGCCATGGCTGTGGCTGGTTT 1274
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Db      1530 CATCGTGGCCGAGCTCTTCAGCCAGGGACCCCGCCCGGCAGCCATGGCTGTGGCTGGTTT 1589

Qy      1275 CTCCAACTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT 1334
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1335 GGGGCCCTACGTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCTTCTTCATCTTCACCTT 1394
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Qy      1395 CTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAGATCTCAGCTGCCTTCCACCG 1454
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Qy      1455 GACACCCTCTCTTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC 1514
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1770 GACACCCTCTCTTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC 1829

Qy      1515 AGATGAGAACGAC 1527
            ||||||||| |||
Db      1830 AGATGAGAATGAC 1842
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Page 3 -> blank

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RESULT 8
CQ730609
LOCUS       CQ730609                2129 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 16543 from Patent WO02068579.
ACCESSION   CQ730609
VERSION     CQ730609.1  GI:42304929
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 16543 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .2129
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             99.8%;  Score 1526.8;  DB 6;  Length 2129;
  Best Local Similarity   99.9%;  Pred. No. 2.8e-313;
  Matches 1528;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCCGTCGGGCTTCCAACAGATAGGCTCCGAAGATGGGGAACCCCCTCAGCAGCGAGTG 60
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